



SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> Chen, Zhijian J.
<120> A KINASE CAPABLE OF SITE SPECIFIC
PHOSPHORYLATION OF IkbA

<130> MPI96-031CP1DV1CPACN1M

<140> 10/052005
<141> 2002-01-17

<150> 09/406293
<151> 1999-09-24

<150> 08/825559
<151> 1997-03-19

<150> 08/616499
<151> 1996-03-19

<160> 9

<170> FastSEQ for Windows Version 4.0
<170> PatentIn Release #1.0, Version #1.30

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<212> DNA
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<400> 3

36

35

Xaa Tyr Val Glu Xaa Glu Arg
1 5

<210> 4
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<210> 6
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Thr Tyr His Ala Leu Ser Asn Leu Pro Lys
1 5 10

<210> 7
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<223> n = any nucleotide

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ccacggtgga  tcagcgccga  cccgagtgtg  cgaagtatgc  caaggaagga  agacttcaag  180
aagtcattga  aacccttctc  tctctggaaa  agcagactcg  tactgcttcc  gatatgggat  240
cgacatcccg  tatcttagtt  gcagtagtga  agntgtgcta  tgaggctaaa  gaatgggatt  300
tacttaatta  aaaatattat  tgctttttgt  ccaaaaggcg  gagtcaagtt  aaaaacaagc  360
tagttgacaa  aaaatggatt  naacagttgc  tgnacttat  tggtt      404

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<210> 8

<211> 323

<212> DNA

<213> homo sapiens

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ccctgagcaa  cctgccgaaa  gcccgagctg  ccttaacttc  ttctcgaacc  acagcaaagt  180
ccatctactg  ccccctaaat  tgcaggccac  cttggacatg  cagtcgggta  ttatccatgc  240
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catcgacagc  ccaaggcatc  aca          323

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<210> 9

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      20      25      30
Gly Leu Asp Ser Met Lys Asp Glu Glu Tyr Glu Gln Met Val Lys Glu
      35      40      45
Leu Gln Glu Ile Arg Leu Glu Pro Gln Glu Val Pro Arg Gly Ser Glu
      50      55      60
Pro Trp Lys Gln Gln Leu Thr Glu Asp Gly Asp Ser Phe Leu His Leu
65      70      75      80
Ala Ile Ile His Glu Lys Ala Leu Thr Met Glu Val Ile Arg Gln
      85      90      95
Val Lys Gly Asp Leu Ala Phe Leu Asn Phe Gln Asn Asn Leu Gln Gln
      100      105      110
Thr Pro Leu His Leu Ala Val Ile Thr Asn Gln Pro Glu Ile Ala Glu
      115      120      125
Ala Leu Leu Gly Ala Gly Cys Asp Pro Glu Leu Arg Asp Phe Arg Gly
      130      135      140
Asn Thr Pro Leu His Leu Ala Cys Glu Gln Gly Cys Leu Ala Ser Val
145      150      155      160
Gly Val Leu Thr Gln Ser Cys Thr Thr Pro His Leu His Ser Ile Leu
      165      170      175
Lys Ala Thr Asn Tyr Asn Gly His Thr Cys Leu His Leu Ala Ser Ile
      180      185      190
His Gly Tyr Leu Gly Ile Val Glu Leu Leu Val Ser Leu Gly Ala Asp
      195      200      205
Val Asn Ala Gln Glu Pro Cys Asn Gly Arg Thr Ala Leu His Leu Ala
      210      215      220
Val Asp Leu Gln Asn Pro Asp Leu Val Ser Leu Leu Lys Cys Gly
225      230      235      240
Ala Asp Val Asn Arg Val Thr Tyr Gln Gly Tyr Ser Pro Tyr Gln Leu
      245      250      255
Thr Trp Gly Arg Pro Ser Thr Arg Ile Gln Gln Gln Leu Gly Gln Leu
      260      265      270

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Thr	Leu	Glu	Asn	Leu	Gln	Met	Leu	Pro	Glu	Ser	Glu	Asp	Glu	Glu	Ser
		275					280					285			
Tyr	Asp	Thr	Glu	Ser	Glu	Phe	Thr	Glu	Phe	Thr	Glu	Asp	Glu	Leu	Pro
	290					295					300				
Tyr	Asp	Asp	Cys	Val	Phe	Gly	Gly	Gln	Arg	Leu	Thr	Leu			
305					310					315					